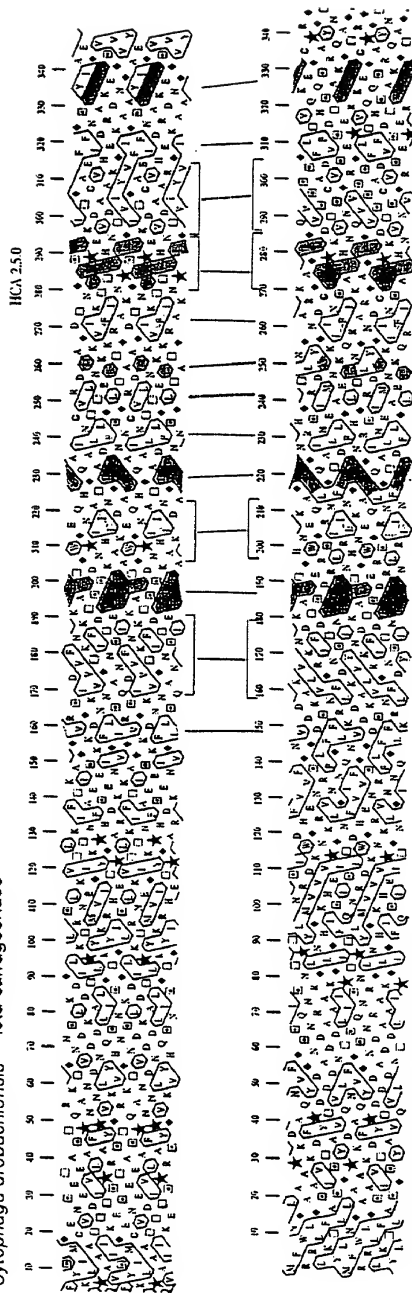


27 AVSPKTYKDAFYVAPTOQDMNY\_\_DLVDDFGANGNDTSD 64  
 28 DISEISEVPTTELRAAASSFYTPPGQNVRRANKKNLVITYGVNHNQND 74  
 65 DSNALQRAINAISRKENGITLLIPNGTYHFLGIQMSNVHRVESDVIIK 114  
 75 DSSKINLAIKDLS\_\_DTGGILILPKGKYLLTKIRMRSNVHLEIEKGIVTY 122  
 115 PTWN GDGKNHRLFVNG\_\_VNNIVRNFSFOGLGNGFLVDFKDSRDKNLAV 161  
 123 PTKGLTPAKNHRIFDFASKTEEKIENASIVGKGGKFTVDLRGNSSKNQIV 172  
 162 FKLGDVRNYKISNFTIDNKTIFASILVDMTERNGRLHWSRNGIITERIKQ 211  
 173 ADVGNVINFKISNFTIKDEKTIIFASILVSFTDKAGN\_AWPHKGIIENIDQ 221  
 212 NNALFGYGLIQTYGADNILFRNLHSEGGIALRMEITDNLMLKNYKQGGIRN 261  
 222 ANAHITGYGLIQAYAADNILFNNLSCTGGVTLRLETIDNLAMKTIKGGVVD 271  
 262 IFADNIRCSKGLAAMVFGPHFMKNGDVQVINVS SVSCGSAVRSDSGFVEL 311  
 272 IFATKIKNINGLTPAMFSPHFMENGKVITDDVTAIGCAYAVRVEHGFTEI 321  
 312 FSPIDEVHTIQSWKQAVESKLRGCAQTPYARGNGGTRWAARVT\_\_OKD 358  
 322 FDKGNRASA\_DAFKNYIEGILGAGSVEVYKRNINGRT\_WAARIANDFNEA 369  
 359 ACLDKAKLEYGIEPGSFGIVKVFDTARF\_GYNADLKQDQLDYFSTSNPM 407  
 370 AYNHSENPAVSGIKPGKFATSKVINVKATYKGTGAKLKQAFLSYLPQSER\_ 418  
 408 CKRVCLPTEKEQWSKQGIYIGPSLAVID\_TTPETSKYDYDVKTENVKRI 457  
 419 SK\_VCRPGPDGFE\_\_YNGPSLGVTIINIKRDNLSLGNVNVNSTSSVQ 462  
 457 NFPVNSHKTIIDINTESSRVONY\_GMSECSSSRWER 491  
 463 GFPNNYVLNVKYNT\_\_PKVCNQNLG\_STTSCN 491

FIG.1

*Cytophaga drobachiensis* iota-carrageenase



*Alteromonas fortis* iota-carrageenase

FIG. 2

1	MKKPNFYGKMGRITALSSLEYLFFLGLVYGQOPTKTSNPNQWTIKWSASDEFN_KNDPDW	59
1	MKPISIVAFPIPAISMLLSAVSQAASM_QPPIAK_PGETWILQAKRSDEFNVK_DAT	55
60	AKWIK_TGNLPNTSAWKWN_NQKNVKISNGIAELTM_RHNANNTPPDGGT_YF	108
56	_KWNFQITENYGVWS_WK_NENAT_V_SNGKLKLTTKRESHQRTFWDGCGNQQVANYPLY	109
109	_TSGIFKSYQKFTYGYFEAKIQGADIGEGVCPFWLYSDFDYSVAN_GETVYSEIDVVVEL	166
110	YTSGVAKSRATGNYGYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGVDVQYSEIDVVVEL	169
167	QOQDWY_EGHODDIYDMDLNLHAVVKENGQGVWKRPKMYPQEQLNKWRAM_DPSKDFHIY	224
170	TQKSAVRES_DH_DLH_NI_VVK_NGKPTWMRPGSFPTQINHNGYHLPDRNDFHTY	221
225	GCEVNQNEIIWYVDGVE_VARKPNKYWHRPMNVTLSLGLRKPFVKFFDNKNNAINPETDA	283
222	GVNVTKDKITWYVDG_EIVGEKONLYWHRQMNLTLSQLRAPHTQW_KCNQFYPSAN	276
284	K_AREKLSDIPTSMYVDYVRVWEKSAGNTTNPPTSEVGTCLKTKGSKLVIDHWDASTGTIS	342
277	KSA_EGF_PTSMEVDYVRTWVKVGNNSAPGEGQSCPNFTFVAVNSVQLSAAKQTLRKG	332
343	AVSNNTKTGQYAGSVNNASIAQIVTLKANTSYKVSAPFGKASSPGTSAYLGISKASNNELI	402
333	QSTTLESTVLPNCATNKKVIYSSSNKNVATVNSAGVV_KAKNKGATITVKTKNKGKIDKL	392
403	SNFEFKTTSYSGEIEIIRTGNVQESYRIWYSSGQAYCDDFNLVEINSGASQLNENETET	462
393	TIAVN	397
463	ALEKGIHIYPNPYKNGPLTIDFGKPFSGEVQITGLNGRTFLRRNVVDQTSVQLLESKSKF	522
523	KSGLIYVKISGPDGEVSKKILVE	545

FIG.3

FIG. 4